



NIEHS SNPs Workshop: Introduction to Workshop and EGP

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Dr. Kenneth Olden, Director of the National Institute of Environmental Health Sciences (NIEHS), convened a historic conference titled "The Environmental Genome Project" on October 17-18, 1997 in Bethesda, Maryland.

Bold Concept:

EGP - Focus on Association Analysis and Environment
Precursor of Many Projects:

NHGRI - Variation Discovery and HapMap
Perlegen

..... 100s of publications using the resources



The EGP is a multi-component project comprised
of research in four areas:

- human DNA polymorphism discovery;
- functional analysis of DNA polymorphism;
- population-based epidemiology studies;
- and technology development.



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Welcome to the NIEHS SNPs Program

Introduction

The NIEHS Environmental Genome Project is a multi-disciplinary, collaborative effort focused on examining the relationships between environmental exposures, inter-individual sequence variation in human genes and disease risk in U.S. populations. The NIEHS SNPs Program at the University of Washington is targeted on the systematic identification and genotyping of single nucleotide polymorphisms (SNPs) in environmental response genes. The first phase of the effort is focused on finding common sequence variation (SNPs) in human genes involved in DNA

Latest Updates to Finished Genes Table	
CDC42BPB	January 12, 2009
CASP8	January 9, 2009
CXB	December 28, 2008
FANCD2	December 27, 2008
MARCKS	December 19, 2008
TRAF4	December 13, 2008
ALDH1A2	December 12, 2008
NEIL3	December 1, 2008
ANAPC10	November 30, 2008
CDKSR2	November 30, 2008
DUSP1	November 30, 2008
IGFBP3	November 30, 2008
MF	November 30, 2008
RETN	November 30, 2008
RXRRA	November 30, 2008
TGFB1	November 30, 2008
CYC1	November 22, 2008



Goals for NIEHS SNPs:

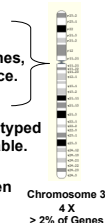
- To identify common sequence variation in genes and pathways that underlie environmental responses
- To provide a variation resource for investigators examining the relationships between environmental exposures, inter-individual sequence variation in human genes and disease risk.

<http://egp.gs.washington.edu>



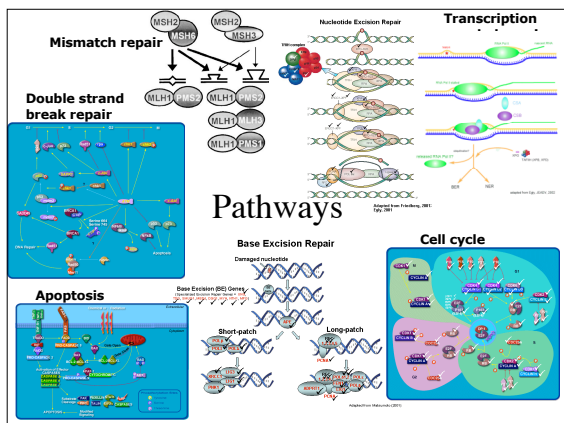
Overview:

- The variation discovery resource complete on 558 genes, more than across 12.9 MB of reference sequence.
- More than 77,000 SNPs have been identified and genotyped in 90-95 samples and 7 million genotypes available.
- Only 50% of the discovered SNPs have previously been described.
- New views are being generated to simplify and enhance use by the community.



Chromosome 3
4X
> 2% of Genes

Bob Livingston
Mark Rieder



Workshop Faculty



NIEHS Workshop Agenda

Day 1:

Finding SNPs I and II
 Mark Rieder and Bob Livingston
 SNP Selection
 Dana Crawford
 Interactive Tutorial I - Database
 Interfaces
 All, led by Mark Rieder and Bob
 Livingston

NIEHS Workshop Agenda

Day 2:

Interactive Tutorial II:
 All, led by Dana Crawford
 SNP Genotyping
 Debbie Nickerson
 Association Analysis
 Chris Carlson
 Medical Resequencing
 Debbie Nickerson
 Resequencing Roundtable
 Bob Livingston

Many Thanks!

David Schwartz - Director
 Sam Wilson - Deputy Director

Liz Maull and Lauranell Burch
 Gwen Collman

Alma Britton
 Jack Field
 Eric Torskey - UW